



OIPE

RAW SEQUENCE LISTING

DATE: 05/13/2002

PATENT APPLICATION: US/10/080,114A

TIME: 16:44:40

Input Set : A:\1301.SEQLIST.TXT

Output Set: N:\CRF3\05132002\J080114A.raw

ENTERED

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7 <110> APPLICANT: Dhugga, Kanwarpal S.
13 <120> TITLE OF INVENTION: Manipulation of Sucrose Synthase Genes
15 to Improve Stalk and Grain Quality
21 <130> FILE REFERENCE: 1301P
25 <140> CURRENT APPLICATION NUMBER: US 10/080,114A
C--> 27 <141> CURRENT FILING DATE: 2002-04-30
31 <150> PRIOR APPLICATION NUMBER: US 60/270,777
33 <151> PRIOR FILING DATE: 2001-02-22
37 <160> NUMBER OF SEQ ID NOS: 13
41 <170> SOFTWARE: FastSEQ for Windows Version 4.0
45 <210> SEQ ID NO: 1
47 <211> LENGTH: 2737
49 <212> TYPE: DNA
51 <213> ORGANISM: Zea mays
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58 cgtcgccctc ctgtccaagt acgtgaacaa ggggaagggc atccgtcagc cgcaaccacat 120
59 cctcgacgcy ctcgacgagc tccagggctc cggggggcgc gcgctagcgc agggaccctt 180
60 cctcgacgtc ctccgctccg cgcagggaggc gatcgtgctg ccgcggttcg tggccatcgc 240
61 ggtgcgcccgc cgcgcgggagc ttggggagta cgtccgctc aacgttccag agctcagcgt 300
62 cgagcagctc acagtctcgg agtaacctcg ctccaaggag gagcttgcg acggccagca 360
63 caatgatccc tacgttctcg agcttgacct cgagccgttc aatgtctcag tcccacgcce 420
64 aaatcggtca tcattatttg gaaacgggtg gcagttcttc aaccgacctc tgtctcaat 480
65 catgttccgc aacagggatt gcttgaggcc cctgttgat ttccctcgtg gccaccggca 540
66 caaggggcat gttatgatc ttaatgatag aatacaaaagc ttggggaggc ttcagctctg 600
67 gctgacaaaa gctgaggagc acttgtcaaa gctccctgct gacacacctc actcaaat 660
68 tgcattaaaa ttccaagagt ggggcctgga gaaaggttgg ggtgatacac caggacaagt 720
69 tttgaaatg atccatctcc ttctagacat cattcagcgc ccagacacctc ctaccctaga 780
70 gaaattcttg gggaggatcc coagtatttt taacgttgtt gtggtatccc ctcaatgga 840
71 ctttggtcaa gctaatgtat taggcttgcc agacacagga ggcagatagc tctatatct 900
72 ggaccaagtc cgtgcactag aaaaatgagat ggttctccgt ttaagaaac agggcgttga 960
73 tgtttcccca aagattctca ttgttactcg gctgatacca gatgcaaaag gaacatcatg 1020
74 caatcagcgc cttgagagaa ttagtggaac acagcataat tacatattac gagttccctt 1080
75 gcaaaatgaa aatgggatac ttaagaaatg gatatacaag ttgatgtgtg ggccatattc 1140
76 ggaacacttt gctgagagtg ctgctggtga aattgctgct gaattacaag gtactccaga 1200
77 ctctataatt agaaactaca gtgattgaaa tcttgtggcg tcattgctat cttaacagat 1260
78 ggaattacc cagtgaacaa ttgctcatgc tctgaaaaag actaagatctc cagattcaga 1320
79 catattttgc aagaatttgc atgagaatga ccattttctc tgccagttca ctgctgatat 1380
80 aattgctgat acaatgtctg attttatcat caccagcaca taccagaaa ttgctggaag 1440
81 caaaaatact gttggacagt atgagagtca tactgccttt actctgcctg gctctgaccg 1500
82 agttgtccat gggatcagtg tcttcgatcc aaagttcaat atagctcttc ctgagctgta 1560
83 catgttcata tactttccac ataccagaaa ggccaaagca ctcacctctc ttcattggtc 1620
84 aatcgaaaat ttgatttatg acccgagaca aaacgatgaa cacattgggc atctggtatg 1680

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85 ccggtcaaaag cccatcctct tctccatggc aagactcgac agggtagaaga acataacagg 1740
86 gctggtcgtaa gcttttgcta agtcgcctaa gctgagggag ctggtaaacc ttgctgcgtg 1800
87 tgccgggttac aatgatgtca acaagtccaa ggacagggaa gagatcgcg agatagagaa 1860
88 gatgcatagaa ctcatcaaga cccacaactt gttccggcgag ttccggtgga tctctgcccc 1920
89 gacaaacagg gcccgtaacg gcgagctcta tcgctacatc gctgataccc atggtgcttt 1980
90 cgtacagcggc gctttgtatg aagcgttcgg tctcaccgtc gttgaggcca tgacctgtgg 2040
91 gcttctact ttcgcgaocg tccatggagg tccagctgag atcatagagc atggcgtctc 2100
92 gggcttccac attgaccggt accaccocga acaggctgtt aatctgagt cgcacttctt 2160
93 cgaccgggtgc aagcaagacc cagatcactg ggtgaatata tctggagcag ggcgcgagcg 2220
94 catatacagag aagtacacat ggaagatata ctgagagagg ttgatgacac tggccggggg 2280
95 ctacgggttcc tggaagtacg tgtcgaagct cgagagggctg gagacgaggc gctaccttga 2340
96 gatgttctac atactgaagt tccgcgagct ggcgaagacc gtgcccgttg caattgacca 2400
97 accgcagtag cttgcgcaac tgcgactgcy tagcacttgg tacaagactg aaacctgaag 2460
98 gaccttcagt aatttaggcy cggcagagcy tagccaataa aatgtgccg agctgaactc 2520
99 gttttttatt atgtacataa tggcagtata acaaaattac tgaaggcagg tgggttgag 2580
100 ttgtgtgttc gttactgttt actgtattat gtoaagctgt cggctgcaat tctttgtctg 2640
101 gcaagccgca ggcactggtg aagtgtctgat aaatacatca tattctgttg acctgtgaaa 2700
102 aaaaaaaaaa aaaaaaaaaa aaaaaaaggc cgccgcgc 2737

106 <210> SEQ ID NO: 2
108 <211> LENGTH: 802
110 <212> TYPE: PRT
112 <213> ORGANISM: Zea mays
116 <400> SEQUENCE: 2

118 Ser Thr His Ala Ser Gly Asp Arg Val Glu Asp Thr Leu His Ala His
119 1 5 10 15
120 Arg Asn Glu Leu Val Ala Leu Leu Ser Lys Tyr Val Asn Lys Gly Lys
121 20 25 30
122 Gly Ile Leu Gln Pro His His Ile Leu Asp Ala Leu Asp Gly Val Gln
123 35 40 45
124 Gly Ser Gly Gly Arg Ala Leu Ala Glu Gly Pro Phe Leu Asp Val Leu
125 50 55 60
126 Arg Ser Ala Gln Glu Ala Ile Val Leu Pro Pro Phe Val Ala Ile Ala
127 65 70 75 80
128 Val Arg Pro Arg Pro Gly Val Trp Glu Tyr Val Arg Val Asn Val His
129 85 90 95
130 Glu Leu Ser Val Glu Gln Leu Thr Val Ser Glu Tyr Leu Arg Phe Lys
131 100 105 110
132 Glu Glu Leu Val Asp Gly Gln His Asn Asp Pro Tyr Val Leu Glu Leu
133 115 120 125
134 Asp Phe Glu Pro Phe Asn Val Ser Val Pro Arg Pro Asn Arg Ser Ser
135 130 135 140
136 Ser Ile Gly Asn Gly Val Gln Phe Leu Asn Arg His Leu Ser Ser Ile
137 145 150 155 160
138 Met Phe Arg Asn Arg Asp Cys Leu Glu Pro Leu Leu Asp Phe Leu Arg
139 165 170 175
140 Gly His Arg His Lys Gly His Val Met Met Leu Asn Asp Arg Ile Gln
141 180 185 190
142 Ser Leu Gly Arg Leu Gln Ser Val Leu Thr Lys Ala Glu Glu His Leu
143 195 200 205

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144 Ser Lys Leu Pro Ala Asp Thr Pro Tyr Ser Gln Phe Ala Tyr Lys Phe
145      210      215      220
146 Gln Glu Trp Gly Leu Glu Lys Gly Trp Gly Asp Thr Ala Gly His Val
147 225      230      235      240
148 Leu Glu Met Ile His Leu Leu Leu Asp Ile Ile Gln Ala Pro Asp Pro
149      245      250      255
150 Ser Thr Leu Glu Lys Phe Leu Gly Arg Ile Pro Met Ile Phe Asn Val
151      260      265      270
152 Val Val Val Ser Pro His Gly Tyr Phe Gly Gln Ala Asn Val Leu Gly
153      275      280      285
154 Leu Pro Asp Thr Gly Gly Gln Ile Val Tyr Ile Leu Asp Gln Val Arg
155      290      295      300
156 Ala Leu Glu Asn Glu Met Val Leu Arg Leu Lys Lys Gln Gly Leu Asp
157 305      310      315      320
158 Val Ser Pro Lys Ile Leu Ile Val Thr Arg Leu Ile Pro Asp Ala Lys
159      325      330      335
160 Gly Thr Ser Cys Asn Gln Arg Leu Glu Arg Ile Ser Gly Thr Gln His
161      340      345      350
162 Thr Tyr Ile Leu Arg Val Pro Phe Arg Asn Glu Asn Gly Ile Leu Lys
163      355      360      365
164 Lys Trp Ile Ser Arg Phe Asp Val Trp Pro Tyr Leu Glu Thr Phe Ala
165      370      375      380
166 Glu Asp Ala Ala Gly Glu Ile Ala Ala Glu Leu Gln Gly Thr Pro Asp
167 385      390      395      400
168 Phe Ile Ile Gly Asn Tyr Ser Asp Gly Asn Leu Val Ala Ser Leu Leu
169      405      410      415
170 Ser Tyr Lys Met Gly Ile Thr Gln Cys Asn Ile Ala His Ala Leu Glu
171      420      425      430
172 Lys Thr Lys Tyr Pro Asp Ser Asp Ile Phe Trp Lys Asn Phe Asp Glu
173      435      440      445
174 Lys Tyr His Phe Ser Cys Gln Phe Thr Ala Asp Ile Ile Ala Met Asn
175      450      455      460
176 Asn Ala Asp Phe Ile Ile Thr Ser Thr Tyr Gln Glu Ile Ala Gly Ser
177 465      470      475      480
178 Lys Asn Thr Val Gly Gln Tyr Glu Ser His Thr Ala Phe Thr Leu Pro
179      485      490      495
180 Gly Leu Tyr Arg Val Val His Gly Ile Asp Val Phe Asp Pro Lys Phe
181      500      505      510
182 Asn Ile Val Ser Pro Gly Ala Asp Met Ser Ile Tyr Phe Pro His Thr
183      515      520      525
184 Glu Lys Ala Lys Arg Leu Thr Ser Leu His Gly Ser Ile Glu Asn Leu
185      530      535      540
186 Ile Tyr Asp Pro Glu Gln Asn Asp Glu His Ile Gly His Leu Asp Asp
187 545      550      555      560
188 Arg Ser Lys Pro Ile Leu Phe Ser Met Ala Arg Leu Asp Arg Val Lys
189      565      570      575
190 Asn Ile Thr Gly Leu Val Glu Ala Phe Ala Lys Cys Ala Lys Leu Arg
191      580      585      590
192 Glu Leu Val Asn Leu Val Val Val Ala Gly Tyr Asn Asp Val Asn Lys

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193          595          600          605
194 Ser Lys Asp Arg Glu Glu Ile Ala Glu Ile Glu Lys Met His Glu Leu
195          610          615          620
196 Ile Lys Thr His Asn Leu Phe Gly Gln Phe Arg Trp Ile Ser Ala Gln
197 625          630          635          640
198 Thr Asn Arg Ala Arg Asn Gly Glu Leu Tyr Arg Tyr Ile Ala Asp Thr
199          645          650          655
200 His Gly Ala Phe Val Gln Pro Ala Leu Tyr Glu Ala Phe Gly Leu Thr
201          660          665          670
202 Val Val Glu Ala Met Thr Cys Gly Leu Pro Thr Phe Ala Thr Leu His
203          675          680          685
204 Gly Gly Pro Ala Glu Ile Ile Glu His Gly Val Ser Gly Phe His Ile
205          690          695          700
206 Asp Pro Tyr His Pro Glu Gln Ala Val Asn Leu Met Ala Asp Phe Phe
207 705          710          715          720
208 Asp Arg Cys Lys Gln Asp Pro Asp His Trp Val Asn Ile Ser Gly Ala
209          725          730          735
210 Gly Leu Gln Arg Ile Tyr Glu Lys Tyr Thr Trp Lys Ile Tyr Ser Glu
211          740          745          750
212 Arg Leu Met Thr Leu Ala Gly Val Tyr Gly Phe Trp Lys Tyr Val Ser
213          755          760          765
214 Lys Leu Glu Arg Leu Glu Thr Arg Arg Tyr Leu Glu Met Phe Tyr Ile
215          770          775          780
216 Leu Lys Phe Arg Glu Leu Ala Lys Thr Val Pro Leu Ala Ile Asp Gln
217 785          790          795          800
218 Pro Gln
224 <210> SEQ ID NO: 3
226 <211> LENGTH: 36
228 <212> TYPE: DNA
230 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
236 <223> OTHER INFORMATION: Designed oligonucleotide based upon the adapter
238 sequence and poly T to remove clones which have a
240 poly A tail but no cDNA.
244 <400> SEQUENCE: 3
246 tcgaccacag cgtccgaaaa aaaaaaaaaa aaaaaa 36
250 <210> SEQ ID NO: 4
252 <211> LENGTH: 2746
254 <212> TYPE: DNA
256 <213> ORGANISM: Zea mays
260 <220> FEATURE:
262 <221> NAME/KEY: CDS
264 <222> LOCATION: (72)...(2480)
268 <400> SEQUENCE: 4
270 aaacctccc tccctctcc attggactgc ttgtccctg ttgaccattg ggtattctga 60
272 accatcgagc c atg gct gcc aag ctg act cgc ctt cac agt ctt cgc gaa 110
274          Met Ala Ala Lys Leu Thr Arg Leu His Ser Leu Arg Glu
276          1          5          10
280 cgc ctt ggt gcc acc ttc tcc tcc oat ccc aat gaa ctg ata gca ctc 158

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282	Arg	Leu	Gly	Ala	Thr	Phe	Ser	Ser	His	Pro	Asn	Glu	Leu	Ile	Ala	Leu	
284		15					20					25					
288	ttt	tcc	agg	tat	ggt	cac	cag	ggc	aag	gga	atg	ctt	cag	cgc	cat	cag	206
290	Phe	Ser	Arg	Tyr	Val	His	Gln	Gly	Lys	Gly	Met	Leu	Gln	Arg	His	Gln	
292	30					35					40				45		
296	ctg	ctt	gcg	gag	ttt	gat	gcc	ctg	ttt	gat	agt	gac	aag	gag	aag	tat	254
298	Leu	Leu	Ala	Glu	Phe	Asp	Ala	Leu	Phe	Asp	Ser	Asp	Lys	Glu	Lys	Tyr	
300						50				55				60			
304	gca	cca	ttt	gaa	gac	att	ctt	cgt	gct	gct	cag	gaa	gca	att	gtg	ctc	302
306	Ala	Pro	Phe	Glu	Asp	Ile	Leu	Arg	Ala	Ala	Gln	Glu	Ala	Ile	Val	Leu	
308				65					70					75			
312	ccc	cca	tgg	gtt	gca	ctt	gct	atc	agg	cca	agg	cct	ggt	gtc	tgg	gat	350
314	Pro	Pro	Trp	Val	Ala	Leu	Ala	Ile	Arg	Pro	Arg	Pro	Gly	Val	Trp	Asp	
316			80					85					90				
320	tac	att	cgg	gtg	aat	gta	agt	gag	ctg	gct	gtg	gag	gag	ctg	agt	gtt	398
322	Tyr	Ile	Arg	Val	Asn	Val	Ser	Glu	Leu	Ala	Val	Glu	Glu	Leu	Ser	Val	
324		95				100					105						
328	tct	gag	tac	ttg	gca	ttc	aag	gaa	cag	ctg	gtg	gat	gga	caa	tcc	aac	446
330	Ser	Glu	Tyr	Leu	Ala	Phe	Lys	Glu	Gln	Leu	Val	Asp	Gly	Gln	Ser	Asn	
332	110					115					120				125		
336	agc	aac	ttt	gtg	ctt	gag	ctt	gat	ttt	gag	ccc	ttc	aat	gcc	tcc	ttt	494
338	Ser	Asn	Phe	Val	Leu	Glu	Leu	Asp	Phe	Glu	Pro	Phe	Asn	Ala	Ser	Phe	
340						130				135				140			
344	cct	cgt	cct	tcc	atg	tcg	aag	tcc	atc	gga	aat	gga	gtg	caa	ttc	ctt	542
346	Pro	Arg	Pro	Ser	Met	Ser	Lys	Ser	Ile	Gly	Asn	Gly	Val	Gln	Phe	Leu	
348				145					150					155			
352	aac	cga	cac	ctg	tcg	tcc	aag	ttg	ttc	cag	gac	aag	gag	agt	ttg	tac	590
354	Asn	Arg	His	Leu	Ser	Ser	Lys	Leu	Phe	Gln	Asp	Ser	Lys	Glu	Ser	Leu	
356			160					165			170						
360	ccc	ttg	ctg	aac	ttc	ctc	aag	gct	cat	aac	tac	aag	ggc	acg	acg	atg	638
362	Pro	Leu	Leu	Asn	Phe	Leu	Lys	Ala	His	Asn	Tyr	Lys	Gly	Thr	Thr	Met	
364		175				180					185						
368	atg	ttg	aat	gac	aga	atc	caa	agc	ctt	cgt	ggt	ctc	caa	tca	tcc	ctg	686
370	Met	Leu	Asn	Asp	Arg	Ile	Gln	Ser	Leu	Arg	Gly	Leu	Gln	Ser	Ser	Leu	
372	190					195					200				205		
376	aga	aag	gca	gag	gag	tat	cta	ctg	agt	gtt	cct	caa	gac	act	ccc	tac	
378	Arg	Lys	Ala	Glu	Glu	Tyr	Leu	Leu	Ser	Val	Pro	Gln	Asp	Thr	Pro	Tyr	734
380					210					215				220			
384	tcg	gag	ttc	aac	cat	agg	ttc	caa	gag	ctt	ggc	ttg	gag	aag	ggt	tggt	782
386	Ser	Glu	Phe	Asn	His	Arg	Phe	Gln	Glu	Leu	Gly	Leu	Glu	Lys	Gly	Trp	
388				225					230					235			
392	ggt	gac	act	gcg	aag	cgt	gtt	ctc	gac	aca	ctc	cac	ttg	ctt	ctc	gac	830
394	Gly	Asp	Thr	Ala	Lys	Arg	Val	Leu	Asp	Thr	Leu	His	Leu	Leu	Leu	Asp	
396			240					245			250						
400	ctt	ctt	gag	gcc	cct	gat	cct	gcc	aac	ttg	gag	aag	ttc	ctt	gga	act	878
402	Leu	Leu	Glu	Ala	Pro	Asp	Pro	Ala	Asn	Leu	Glu	Lys	Phe	Leu	Gly	Thr	
404		255				260					265						
408	ata	cca	atg	atg	ttc	aac	gtt	gtt	atc	ctg	tct	cct	cat	ggc	tac	ttc	926
410	Ile	Pro	Met	Met	Phe	Asn	Val	Val	Ile	Leu	Ser	Pro	His	Gly	Tyr	Phe	

VERIFICATION SUMMARY

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L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1452 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11
L:1460 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:11